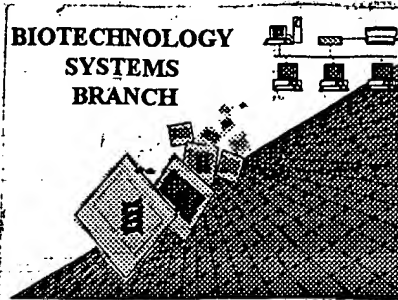


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/742,454

Source: OIPE

Date Processed by STIC: 1/11/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/742,454

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) 2,7. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's, Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

No = 2

RAW SEQUENCE LISTING DATE: 01/11/2001
 PATENT APPLICATION: US/09/742,454 TIME: 16:50:08

Input Set : A:\2968-B.txt
 Output Set: N:\CRF3\01112001\I742454.raw

Does Not Comply
 Corrected Diskette Needed

PP. 2, 4

OK

```

3 <110> APPLICANT: WILEY, Steven R.
5 <120> TITLE OF INVENTION: TWEAK Receptor
7 <130> FILE REFERENCE: 2968-B
9 <140> CURRENT APPLICATION NUMBER: US/09/742,454
10 <141> CURRENT FILING DATE: 2000-12-19
12 <150> PRIOR APPLICATION NUMBER: 60/172,878
13 <151> PRIOR FILING DATE: 1999-12-20
15 <150> PRIOR APPLICATION NUMBER: 60/203,347
16 <151> PRIOR FILING DATE: 2000-05-10
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 898
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (52)..(873)
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
33 fusion protein construct
35 <400> SEQUENCE: 1
36 tctcgagggc cagcggttta aacgtcgagg tacctatccc gggccgccac c atg gct 57
37 Met Ala
38 1
40 aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
41 Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
42 5 10 15
44 ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
45 Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
46 20 25 30
48 ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
49 Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
50 35 40 45 50
52 aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
53 Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
54 55 60 65
56 agt ttg ggg agc cgg gca tgc ctg tcc gcc cag gag cct gcc cag gag 297
57 Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu
58 70 75 80
60 gag ctg gtg gca gag gag gac cag gac ccg tgc gaa ctg aat ccc cag 345
61 Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln
62 85 90 95
64 aca gaa gaa agc cag gat cct gcg cct ttc ctg aac cga cta gtt cgg 393
65 Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg
66 100 105 110
68 cct cgc aga agt gca cct aaa ggc cgg aaa aca cgg gct cga aga gcg 441
  
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/742,454

DATE: 01/11/2001

TIME: 16:50:08

Input Set : A:\2968-B.txt

Output Set: N:\CRF3\01112001\I742454.raw

```

69 Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala
70 115 120 125 130
72 atc gca gcc cat tat gaa gtt cat cca cga cct gga cag gac gga gcg 489
73 ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala
74 135 140 145
76 cag gca ggt gtg gac ggg aca gtg agt ggc tgg gag gaa gcc aga atc 537
77 Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile
78 150 155 160
80 aac agc tcc agc cct ctg cgc tac aac cgc cag atc ggg gag ttt ata 585
81 Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile
82 165 170 175
84 gtc acc cgg gct ggg ctc tac ctg tac tgt cag gtg cac ttt gat 633
85 Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp
86 180 185 190
88 gag ggg aag gct gtc tac ctg aag ctg gac ttg ctg gtg gat ggt gtg 681
89 Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val
90 195 200 205 210
92 ctg gcc ctg cgc tgc ctg gag gaa ttc tca gcc act gcg gcc agt tcc 729
93 Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser
94 215 220 225
96 ctc ggg ccc cag ctc cgc ctc tgc cag gtg tct ggg ctg ttg gcc ctg 777
97 Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu
98 230 235 240
100 cgg cca ggg tcc tcc ctg cgg atc cgc acc ctc ccc tgg gcc cat ctc 825
101 Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu
102 245 250 255
104 aag gct gcc ccc ttc ctc acc tac ttc gga ctc ttc cag gtt cac tga 873
105 Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
106 260 265 270
108 gcggcgcggg atctgttttaa actag 898
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 273
113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence
W--> 116 <220> FEATURE:
W--> 116 <223> OTHER INFORMATION:
116 <100> SEQUENCE: 2
117 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
118 1 5 10 15
120 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met
121 20 25 30
123 Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
124 35 40 45
126 Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
127 50 55 60
129 Arg Ser Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala
130 65 70 75 80
132 Gln Glu Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn
133 85 90 95

```

→ see item 7 on Error Summary Sheet

This error also
appears in
sequence 7.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/742,454
 DATE: 01/11/2001
 TIME: 16:50:08

Input Set : A:\2968-B.txt
 Output Set: N:\CRF3\01112001\I742454.raw

```

135 Pro Gln Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu
136          100          105          110
138 Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg
139          115          120          125
141 Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
142          130          135          140
144 Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala
145 145          150          155          160
147 Arg Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu
148          165          170          175
150 Phe Ile Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
151          180          185          190
153 Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp
154          195          200          205
156 Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
157          210          215          220
159 Ser Ser Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
160 225          230          235          240
162 Ala Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
163          245          250          255
165 His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
166          260          265          270
168 His
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 868
173 <212> TYPE: DNA
174 <213> ORGANISM: Homo sapiens
176 <220> FEATURE:
177 <221> NAME/KEY: CDS
178 <222> LOCATION: (53)..(442)
180 <400> SEQUENCE: 3
181 gcttgaattc aataactata acggtcctaa ggtagcgaag aggacgtgca ct atg gct 58
182                                     Met Ala
183                                     1
185 cgg ggc tgg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106
186 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
187          5          10          15
189 ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca gcc acc gcc 154
190 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
191          20          25          30
193 ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
194 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
195 35          40          45          50
197 gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
198 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly
199          55          60          65
201 tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
202 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu
203          70          75          80

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/742,454

DATE: 01/11/2001

TIME: 16:50:08

Input Set : A:\2968-B.txt

Output Set: N:\CRF3\01112001\I742454.raw

205 ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
 206 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
 207 85 90 95
 209 ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394
 210 Leu Val Trp Arg Arg Cys Arg Arg Glu Lys Phe Thr Thr Pro Ile
 211 100 105 110
 213 gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
 214 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
 W--> 215 115 120 125 (130) *delete, since no amino acid is present*
 217 caatgtgcc cctgccagcc ggggctgcc cactcatcat tcatcatcat attctagagc 502
 219 cagtcctctgc ctcccagacy cggcgggagc caagctcctc caaccacaag gggggtggg 562
 221 ggcgggtgaat cactctctgag gcctggggccc agggttcagg ggaaccttcc aaggtgtctg 622
 223 gttgccctgc ctctggctcc agaacagaaa gggagcctca cgctggctca cacaaaacag 682
 225 ctgacactga ctaaggaact gcagcatttg cacaggggag ggggggtgcc tcttctctag 742
 227 aggcctctgg ggcaggtctg acttgggggg cagacttgac actagggccc actcactcag 802
 229 atgtctctgaa attccaccac gggggtcacc ctggggggtt agggacctat ttttaacact 862
 231 agagggg 868
 234 <210> SEQ ID NO: 4
 235 <211> LENGTH: 129
 236 <212> TYPE: PRT
 237 <213> ORGANISM: Homo sapiens
 239 <400> SEQUENCE: 4
 240 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
 241 1 5 10 15
 243 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 244 20 25 30
 246 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 247 35 40 45
 249 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 250 50 55 60
 252 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 253 65 70 75 80
 255 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 256 85 90 95
 258 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 259 100 105 110
 261 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 262 115 120 125
 264 Gln
 267 <210> SEQ ID NO: 5
 268 <211> LENGTH: 129
 269 <212> TYPE: PRT
 270 <213> ORGANISM: Mus sp.
 272 <400> SEQUENCE: 5
 273 Met Ala Pro Gly Trp Pro Arg Ser Leu Pro Gln Ile Leu Val Leu Gly
 274 1 5 10 15
 276 Phe Gly Leu Val Leu Met Arg Ala Ala Ala Gly Glu Gln Ala Pro Gly
 277 20 25 30
 279 Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys

RAW SEQUENCE LISTING

DATE: 01/11/2001

PATENT APPLICATION: US/09/742,454

TIME: 16:50:08

Input Set : A:\2968-B.txt

Output Set: N:\CRF3\01112001\I742454.raw

```

280          35          40          45
282 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys
283          50          55          60
285 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro
286 65          70          75          80
288 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser
289          85          90          95
291 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
292          100          105          110
294 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile
295          115          120          125
297 Gln
301 <210> SEQ ID NO: 6
302 <211> LENGTH: 932
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (1)..(930)
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
312     receptor fusion protein construct
314 <400> SEQUENCE: 6
315 atg gct cgg ggc tgg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg 48
316 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
317 1          5          10          15
319 ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc 96
320 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
321          20          25          30
323 acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag 144
324 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
325          35          40          45
327 tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc 192
328 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
329          50          55          60
331 ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga 240
332 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
333 65          70          75          80
335 tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc 288
336 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
337          85          90          95
339 gag ggc gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc 336
340 Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
341          100          105          110
343 ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg 384
344 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
345          115          120          125
347 agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg 432
348 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

```

VERIFICATION SUMMARY

DATE: 01/11/2001

PATENT APPLICATION: US/09/742,454

TIME: 16:50:09

Input Set : A:\2968-B.txt

Output Set: N:\CRF3\01112001\I742454.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:116 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:116 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:401 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:401 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: